

Figure 1 (A)

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGGGCAGGTATCTTGGCTCACAGGGGA																				79
M	S	S	S	S	W	L	L	L	S	L	V	A	V	T	A	A	Q	S		19
CG	ATG	TCA	AGC	TCT	TCC	TGG	CTC	CTT	CTC	AGC	CTT	GTT	GCT	GTA	ACT	GCT	GCT	CAG	TCC	138
T	I	E	E	Q	A	K	T	F	L	D	K	F	N	H	E	A	E	D	L	39
ACC	ATT	GAG	GAA	CAG	GCC	AAG	ACA	TTT	TTG	GAC	AAG	TTT	AAC	CAC	GAA	GCC	GAA	GAC	CTG	198
F	Y	Q	S	S	L	A	S	W	N	Y	N	T	N	I	T	E	E	N	V	59
TTC	TAT	CAA	AGT	TCA	CTT	GCT	TCT	TGG	AAT	TAT	AAC	ACC	AAT	ATT	ACT	GAA	GAG	AAT	GTC	258
Q	N	M	N	N	A	G	D	K	W	S	A	F	L	K	E	Q	S	T	L	79
CAA	AAC	ATG	AAT	AAT	GCT	GGG	GAC	AAA	TGG	TCT	GCC	TTT	TTA	AAG	GAA	CAG	TCC	ACA	CTT	318
A	Q	M	Y	P	L	Q	E	I	Q	N	L	T	V	K	L	Q	L	Q	A	99
GCC	CAA	ATG	TAT	CCA	CTA	CAA	GAA	ATT	CAG	AAT	CTC	ACA	GTC	AAG	CTT	CAG	CTG	CAG	GCT	378
L	Q	Q	N	G	S	S	V	L	S	E	D	K	S	K	R	L	N	T	I	119
CTT	CAG	CAA	AAT	GGG	TCT	TCA	GTG	CTC	TCA	GAA	GAC	AAG	AGC	AAA	CGG	TTG	AAC	ACA	ATT	438
L	N	T	M	S	T	I	Y	S	T	G	K	V	C	N	P	D	N	P	Q	139
CTA	AAT	ACA	ATG	AGC	ACC	ATC	TAC	AGT	ACT	GGA	AAA	GTT	TGT	AAC	CCA	GAT	AAT	CCA	CAA	498
E	C	L	L	L	E	P	G	L	N	E	I	M	A	N	S	L	D	Y	N	159
GAA	TGC	TTA	TTA	CTT	GAA	CCA	GGT	TTG	AAT	GAA	ATA	ATG	GCA	AAC	AGT	TTA	GAC	TAC	AAT	558
E	R	L	W	A	W	E	S	W	R	S	E	V	G	K	Q	L	R	P	L	179
GAG	AGG	CTC	TGG	GCT	TGG	GAA	AGC	TGG	AGA	TCT	GAG	GTC	GGC	AAG	CAG	CTG	AGG	CCA	TTA	618
Y	E	E	Y	V	V	L	K	N	E	M	A	R	A	N	H	Y	E	D	Y	199
TAT	GAA	GAG	TAT	GTG	GTC	TTG	AAA	AAT	GAG	ATG	GCA	AGA	GCA	AAT	CAT	TAT	GAG	GAC	TAT	678
G	D	Y	W	R	G	D	Y	E	V	N	G	V	D	G	Y	D	Y	S	R	219
GGG	GAT	TAT	TGG	AGA	GGA	GAC	TAT	GAA	GTA	AAT	GGG	GTA	GAT	GGC	TAT	GAC	TAC	AGC	CGC	738
G	Q	L	I	E	D	V	E	H	T	F	E	E	I	K	P	L	Y	E	H	239
GGC	CAG	TTG	ATT	GAA	GAT	GTG	GAA	CAT	ACC	TTT	GAA	GAG	ATT	AAA	CCA	TTA	TAT	GAA	CAT	798
L	H	A	Y	V	R	A	K	L	M	N	A	Y	P	S	Y	I	S	P	I	259
CTT	CAT	GCC	TAT	GTG	AGG	GCA	AAG	TTG	ATG	AAT	GCC	TAT	CCT	TCC	TAT	ATC	AGT	CCA	ATT	858
G	C	L	P	A	H	L	L	G	D	M	W	G	R	F	W	T	N	L	Y	279
GGA	TGC	CTC	CCT	GCT	CAT	TTG	CTT	GGT	GAT	ATG	TGG	GGT	AGA	TTT	TGG	ACA	AAT	CTG	TAC	918
S	L	T	V	P	F	G	Q	K	P	N	I	D	V	T	D	A	M	V	D	299
TCT	TTG	ACA	GTT	CCC	TTT	GGA	CAG	AAA	CCA	AAC	ATA	GAT	GTT	ACT	GAT	GCA	ATG	GTG	GAC	978
Q	A	W	D	A	Q	R	I	F	K	E	A	E	K	F	F	V	S	V	G	319
CAG	GCC	TGG	GAT	GCA	CAG	AGA	ATA	TTC	AAG	GAG	GCC	GAG	AAG	TTT	TTT	GTA	TCT	GTT	GGT	1038
L	P	N	M	T	Q	G	F	W	E	N	S	M	L	T	D	P	G	N	V	339
CTT	CCT	AAT	ATG	ACT	CAA	GGA	TTC	TGG	GAA	AAT	TCC	ATG	CTA	ACG	GAC	CCA	GGA	AAT	GTT	1098
Q	K	A	V	C	H	P	T	A	W	D	L	G	K	G	D	F	R	I	L	359
CAG	AAA	GCA	GTC	TGC	CAT	CCC	ACA	GCT	TGG	GAC	CTG	GGG	AAG	GGC	GAC	TTC	AGG	ATC	CTT	1158
M	C	T	K	V	T	M	D	D	F	L	T	A	H	H	E	M	G	H	I	379
ATG	TGC	ACA	AAG	GTG	ACA	ATG	GAC	GAC	TTC	CTG	ACA	GCT	CAT	CAT	GAG	ATG	GGG	CAT	ATC	1218
Q	Y	D	M	A	Y	A	A	Q	P	F	L	L	R	N	G	A	N	E	G	399
CAG	TAT	GAT	ATG	GCA	TAT	GCT	GCA	CAA	CCT	TTT	CTG	CTA	AGA	AAT	GGA	GCT	AAT	GAA	GGA	1278
F	H	E	A	V	G	E	I	M	S	L	S	A	A	T	P	K	H	L	K	419
TTC	CAT	GAA	GCT	GTT	GGG	GAA	ATC	ATG	TCA	CTT	TCT	GCA	GCC	ACA	CCT	AAG	CAT	TTA	AAA	1338
S	I	G	L	L	S	P	D	F	Q	E	D	N	E	T	E	I	N	F	L	439
TCC	ATT	GGT	CTT	CTG	TCA	CCC	GAT	TTT	CAA	GAA	GAC	AAT	GAA	ACA	GAA	ATA	AAC	TTC	CTG	1398
L	K	Q	A	L	T	I	V	G	T	L	P	F	T	Y	M	L	E	K	W	459
CTC	AAA	CAA	GCA	CTC	ACG	ATT	GTT	GGG	ACT	CTG	CCA	TTT	ACT	TAC	ATG	TTA	GAG	AAG	TGG	1458
R	W	M	V	F	K	G	E	I	P	K	D	Q	W	M	K	K	W	W	E	479
AGG	TGG	ATG	GTC	TTT	AAA	GGG	GAA	ATT	CCC	AAA	GAC	CAG	TGG	ATG	AAA	AAG	TGG	TGG	GAG	1518

ZBD

Figure 1(B)

M K R E I V G V V E P V P H D E T Y C D 499  
 ATG AAG CGA GAG ATA GTT GGG GTG GTG GAA CCT GTG CCC CAT GAT GAA ACA TAC TGT GAC 1578  
 P A S L F H V S N D Y S F I R Y Y T R T 519  
 CCC GCA TCT CTG TTC CAT GTT TCT AAT GAT TAC TCA TTC ATT CGA TAT TAC ACA AGG ACC 1638  
 L Y Q F Q F Q E A L C Q A A K H E G F L 539  
 CTT TAC CAA TTC CAG TTT CAA GAA GCA CTT TGT CAA GCA GCT AAA CAT GAA GGC CCT CTG 1698  
 H K C D I S N S T E A G Q K L F N M L R 559  
 CAC AAA TGT GAC ATC TCA AAC TCT ACA GAA GCT GGA CAG AAA CTG TTC AAT ATG CTG AGG 1758  
 L G K S E P W T L A L E N V V G A K N M 579  
 CTT GGA AAA TCA GAA CCC TGG ACC CTA GCA TTG GAA AAT GTT GTA GGA GCA AAG AAC ATG 1818  
 N V R P L L N Y F E P L F T W L K D Q N 599  
 AAT GTA AGG CCA CTG CTC AAC TAC TTT GAG CCC TTA TTT ACC TGG CTG AAA GAC CAG AAC 1878  
 K N S F V G W S T D W S P Y A D Q S I K 619  
 AAG AAT TCT TTT GTG GGA TGG AGT ACC GAC TGG AGT CCA TAT GCA GAC CAA AGC ATC AAA 1938  
 V R I S L K S A L G D K A Y E W N D N E 639  
 GTG AGG ATA AGC CTA AAA TCA GCT CTT GGA GAT AAA GCA TAT GAA TGG AAC GAC AAT GAA 1998  
 M Y L F R S S V A Y A M R Q Y F L K V K 659  
 ATG TAC CTG TTC CGA TCA TCT GTT GCA TAT GCT ATG AGG CAG TAC TTT TTA AAA GTA AAA 2058  
 N Q M I L F G E E D V R V A N L K P R I 679  
 AAT CAG ATG ATT CTT TTT GGG GAG GAG GAT GTG CGA GTG GCT AAT TTG AAA CCA AGA ATC 2118  
 S F N F F V T A P K N V S D I I F R T E 699  
 TCC TTT AAT TTC TTT GTC ACT GCA CCT AAA AAT GTG TCT GAT ATC ATT CCT AGA ACT GAA 2178  
 V E K A I R M S R S R I N D A F R L N D 719  
 GTT GAA AAG GCC ATC AGG ATG TCC CGG AGC CGT ATC AAT GAT GCT TTC CGT CTG AAT GAC 2238  
 N S L E F L G I Q P T L G P P N Q P F V 739  
 AAC AGC CTA GAG TTT CTG GGG ATA CAG CCA ACA CTT GGA CCT CCT AAC CAG CCC CCT GTT 2299  
 S I W L I V F G V V M G V I V V G I V I 759  
 TCC ATA TGG CTG ATT GTT TTT GGA GTT GTG ATG GGA GTG ATA GTG GTT GGC ATT GTC ATC 2358  
 L I F T G I R D R K K K N K A R S G E N 779  
 CTG ATC TTC ACT GGG ATC AGA GAT CGG AAG AAG AAA AAT AAA GCA AGA AGT GGA GAA AAT 2418  
 P Y A S I D I S K G E N N P G F Q N T D 799  
 CCT TAT GCC TCC ATC GAT ATT AGC AAA GGA GAA AAT AAT CCA GGA TTC CAA AAC ACT GAT 2478  
 D V Q T S F \* 806  
 GAT GTT CAG ACC TCC TTT TAG 2499  
 AAAAATCTATGTTTTTCTCTTGTAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGGTATAGAAAATATAAGATGAT 2578  
 AAAGATATCATTAAATGTCAAACTATGACTCTGTTTCAGAAAAAAATGTCCAAAGACAACATGGCCAAGGAGAGAGC 2657  
 ATCTTCATTGACATTGCTTTTCAGTATTTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGT 2736  
 ATTAGAGTATATTAGGGAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAATGTAATGTCTGTTGAAT 2815  
 TTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTGGATCTTGATGGAATATGGATGGATCACTTGTAAGG 2894  
 ACAGTGCCTGGGAAGTGGTGTAGCTGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTTCATTTAATCCATTGTCAAG 2973  
 GATGACATGCTTTCTTCACAGTAAGTCAAGTCAAGTACTATGGTGAATTTGCCTACAGTGATGTTTGGAAATCGATCATGC 3052  
 TTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAAATCCAGGGAACAGGTAGAGGACATTGCTTTTCACTTCCAAGGTGC 3131  
 TTGATCAACATCTCCCTGACAACACAAAAGTAGAGCCAGGGGCTCCGTGAAGTCCCAGAGCATGCCTGATAGAACTC 3210  
 ATTTCTACTGTTCTCTAACTGTGGAGTGAATGGAATTCCTCAAGTGTATGTTTACCCTCTGAAGTGGGTACCCAGTCTCT 3289  
 TAAATCTTTTGTATTTGCTCACAGTGTGTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAAATGCTAGATTTACACA 3368  
 CTCAAAAAAGGGCGCCGC 3396

TMD

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**Figure 2 (A)**

ace-2  
hu-ACET  
mu-ACET  
rb-ACET  
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mu-ACE  
rat-ACE  
rb-ACE

MGAASGRGPGLLLLPLP-----LLLLL-PQFALALDPGLQPGNFSAD~~E~~AGAQLFAQSYN  
MGAASGQRGRWFLSPPLMLSLVLVLLQP-SFAPALDPGLQPGNFSF~~E~~AGAQLFAESYN  
MGAASGQRGRWFLSPPLMLSLLLLLLLPPSPAPALDPGLQPGNFSAD~~E~~AGAQLFADSYN  
MGAAPGRGRPRLLRPPPL-LLLLLLRPPPAALTLD~~E~~GLLPDGFAD~~E~~AGARLFASSYN

ace-2  
hu-ACET  
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SSAEQVLFSVAASWAHDTNITAENARRQEEAALLSQEFAEWGQKAKELYEPIWQNFTD  
SSAEVVMFQSTVASWAHDTNITEENARRQEEAALLSQEFAEVWGKKAKELYESIWNFTD  
SSAEVVMFQSTAASWAHDTNITEENARLQEEAALINQFAEVWGKKAKELYESIWNFTD  
SSAEQVLFIRSTAASWAHDTNITAENARRQEEAALLSQEFAEWGRRLLSSMTRCGRTSFT

ace-2  
hu-ACET  
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rb-ACE

FQLRRIIGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTAKVCLFNKATCWSLDPDLTN  
SKLRIIGSIRTLGPANLPLAQRQQYNALLSNMSRIYSTGKVCFPNKATCWSLDPDLTN  
QKLRIIGSVQTLGPANLPLTQRLQYNALLSNMSRIYSTGKVCFPNKATCWSLDPDLTN  
QSCAGSSGLCAFWFCQPAF-GQAAADNALLSNMSQIYSTGRSASFTRLPAFWSLDPDLNN

ace-2  
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ILASSRSYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFSTGAYWRSWYNSP  
ILASSRSYAKLLFAWEGWHDAVGIPLKPLYQDFTALSNEAYRQDGFSTGAFWRSWYESP  
ILASSRNYAKVLLFAWEGWHDAVGIPLRPLYQDFTALSNEAYRQDGFSTGAYWRSWYESP  
ILASSRSYAMLLFAWEGWHNAVGIPLKPLYQDFTALSNEAYRQDGFSTGAYWRSWYDSP

ace-2  
hu-ACET  
mu-ACET  
rb-ACET  
hu-ACE  
mu-ACE  
rat-ACE  
rb-ACE

TFEDDLEHLYQOLEPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLGDMWAQSWENIY  
SFEESLEHIYHQLEPLYLNLHAYVRRALHRRYGDKYVNLRGPIPAHLGDMWAQSWENIY  
SFEESLEHLYHQVEPLYLNLHAFVRRALHRRYGDKYINLRGPIPAHLGDMWAQSWENIY  
TFEEDLERIYHQLEPLYLNLHAYVRRVLHRRYGDRYINLRGPIPAHLGNMWAQSWESIY

ace-2  
hu-ACET  
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rb-ACET  
hu-ACE  
mu-ACE  
rat-ACE  
rb-ACE

DMVVPPFDKPNLDVSTMLQGGWNATHMFRVAEEFFTSLELSPMPPEFWAGSMLEKPADG  
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVSEFFTSGLSPMPPEFWAESMLEKPTDG  
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVAEEFFTSGLSPMPPEFWAESMLEKPADG  
DMVVPPFDKPNLDVSTMVQKGWNATHMFRVAEEFFTSGLLPMPEFWAESMLEKPEDG

ace-2  
hu-ACET  
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rb-ACET  
hu-ACE  
mu-ACE  
rat-ACE  
rb-ACE

REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHIQYYLQYKDLFVSLRRGANP  
REVVCHASAWDFYNRKDFRIKQCTRVMEQLATVHHMGHVQYYLQYKDLHVSLLRRGANP  
REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHVQYYLQYKDLHVSLLRRGANP  
REVVCHASAWDFYNRKDFRIKQCTQVTMDQLSTVHHMGHVQYYLQYKQDFVSLRR-ANP

Figure 2 (B)

ace-2  
hu-ACET  
mu-ACET  
rb-ACET  
hu-ACE  
mu-ACE  
rat-ACE  
rb-ACE

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GFHEAIGDVLALS SVSTFEHLHKIGLLDRVTNDTESDINYLKMALEKIAFLPFGYLVDQW  
GFHEAIGDVLALS SVSTFAHLHKIGLLDHVTNDIESDINYLKMALEKIAFLPFGYLVDQW  
GFHEAIGDVLALS SVSTFAHLHKIGLLDRVANDIESDINYLKMALEKIAFLPFGYLVDQW  
GFHEAIGDVLALS SVSTFAHLHKIGLLDHVTNDTESDINYLKMALEKIAFLPFGYLVDQW

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hu-ACET  
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mu-ACE  
rat-ACE  
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RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVFNVTPIRYFVSF  
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHVFNVTPIRYFVSF  
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHVFNVTPIRYFVSF  
RWGVFSGRTPPSRYNFDWWYLRTKYQGICPPVARNETHFDAGAKFHVFNVTPIRYFVSF

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hu-ACET  
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-----  
-----MGQGWATAGLP SLLFLLLC  
-----MGQGWATPGLPSFLFL---LC  
-----MGQGWAPGLPSLL LLLCCGHSLL  
VLQFQFHEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLQAGSSRPWQEV LKDMVGLDAL  
VLQFQFHQALCKEAGHQGFLHQCDIYQSTQAGAKLKQVLQAGCSR PWQEV LKDLVGS DAL  
VLQFQFHQALCKEAGHQGFLHQCDIYQSTKAGAKLQV LQAGCSR PWQEV LKDLVGS DAL  
VLQFQFHQALCKEAGHQGFLHQCDIYQSTRAGAKLRAVLQAGCSR PWQEV LKDMVGS DAL

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-----MSSSWLLLSLVAVTAA---QSTIEEQAKTFL  
YGHPLLVFSQEASQQVTVTHTGTSQATTSSQTTTHQATAHQTSAQSFNLVTDEAEASRFV  
CGHLLLVLSQVATDHVTANQGITNQATTSQTTHQATIDQTTQI-FNLETDEAKADRFV  
VPSRVAARRVTVNQGTTSQATTSKATTSIRATTHQTTHQATTSQSFNLVTDEAEASRFV  
DAQPLLLKYFQPVTVLQEQNQNGEVLGWPEYQWHFPLPDNYPEG-IDLVTDEAEASRFV  
DAKALLEYFQPVSQWLEEQNQNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKADRFV  
DASALMEYFQPVSQWLEEQNQNGEVLGWPEYQWRPPLPDNYPEG-IDLETDEAKADRFV  
DAQPLLDYFQPVTVLQEQNERNGEVLGWPEYQWRPPLPDNYPEG-IDLVTDEAEASRFV  
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ace-2  
hu-ACET  
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rat-ACE  
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DKFNHEAEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQSTLAQMYFLOEIQ  
EEYDRTSQVWVNEYAEANWNYNTNITETSKILLQKNMQIANHTLKYGTQARKFDVNLQ  
EEYDRTAQVLLNEYAEANWNYNTNITIEGSKILLEKSTEVSNHTLKYGTQARKFDVSNFQ  
EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNWARREFDVSNFQ  
EEYDRTSQVWVNEYAEANWNYNTNITETSKILLQKNMQIANHTLKYGTQARKFDVNLQ  
EEYDRTAQVLLNEYAEANWNYNTNITIEGSKILLEKSTEVSNHTLKYGTQARKFDVSNFQ  
EEYDRTAKVWVNEYAEANWNYNTNITIEGSKILLQKNKEVSNHTLKYGTWAKTFDVSNFQ  
EEYDRSFQAVWVNEYAEANWNYNTNITTEASKILLQKNMQIANHTLTYGNWARREFDVSNFQ  
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ace-2  
hu-ACET  
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NLTVKLQALQOQNGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQECLELLEPGLN  
NTTIKRIIKKVQDLERAAALPAQELEEYNKILLDMETTSVATVCHPNG--SCLQLEPDLT  
NSSIKRIIKKLQNLDRAVLPKPELEEYNQILLDMETTSVATVCHPNG--TCMPLEPDLT  
NATSKRIIKKVQDLQRAVLVPKPELEEYNQILLDMETTSVATVCHPNG--SCLQLEPDLT  
NTTIKRIIKKVQDLERAAALPAQELEEYNKILLDMETTSVATVCHPNG--SCLQLEPDLT  
NSSIKRIIKKLQNLDRAVLPKPELEEYNQILLDMETTSVATVCHPNG--TCMPLEPDLT  
NSTIKRIIKKVQDLQRAVLVPKPELEEYNQILLDMETTSVATVCHPNG--TCMPLEPDLT  
NATSKRIIKKVQDLQRAVLVPKPELEEYNQILLDMETTSVATVCHPNG--SCLQLEPDLT  
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ace-2  
hu-ACET  
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EIMANSIDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDYGDYWRGDYEV  
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQARLNGYVDAGDSWRSMYET  
NMMATSRKYEDLLWAWKSWRDKVGRAILPFPKYVEFSNKIAKLNGYTDAGDSWRSLYES  
NLMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET  
NVMATSRKYEDLLWAWEGWRDKAGRAILQFYPKYVELINQARLNGYVDAGDSWRSMYET  
NMMATSRKYEDLLWAWKSWRDKVGRAILPFPKYVEFSNKIAKLNGYTDAGDSWRSLYES  
NIMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET  
NLMATSRKYEDLLWVWTSWRDKVGRAILPFPKYVEFTNKAARLNGYVDAGDSWRSMYET  
: : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \* . : \*

Figure 2 (C)

ace-2 NGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPIGCLPAHLLG  
 hu-ACET P-----SLEQDLERLFQELQPLYLNLHAYVRRALHRRHYGAQHINLEGPIPAHLLG  
 mu-ACET D-----NLEQDLEKLYQELQPLYLNLHAYVRRSLHRRHYGAQHINLEGPIPAHLLG  
 rb-ACET P-----TLEQDLERLFQELQPLYLNLHAYVRRALHRRHYGAQHINLEGPIPAHLLG  
 hu-ACE P-----SLEQDLERLFQELQPLYLNLHAYVRRALHRRHYGAQHINLEGPIPAHLLG  
 mu-ACE D-----NLEQDLEKLYQELQPLYLNLHAYVRRSLHRRHYGSEYINLDGPIPAHLLG  
 rat-ACE D-----DLEQDLEKLYQELQPLYLNLHAYVRRSLHRRHYGSEYINLDGPIPAHLLG  
 rb-ACE P-----TLEQDLERLFQELQPLYLNLHAYVGRALHRRHYGAQHINLEGPIPAHLLG  
 \* :\*: :\*: :\*: :\*: :\*: :\* . \* . . . \* :\*\*\*\*\*

ace-2 DMWGREWTNLYSLTVFPGQKPNIDVTAMVDQAWDAQRI FKEAEKFVSVGLPNMTQGF  
 hu-ACET NMWAQTWSNIYDLVVPFSPASMDTTEAMLKQGWTPRRMFKEADDFTSGLLLPVPPEFW  
 mu-ACET NMWAQTWSNIYDLVVPFSPAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLLPVPPEFW  
 rb-ACET NMWAQTWSNIYDLVVPFSPASTMDATEAMIKQGWTPRRMFEEADKFFISGLLLPVPPEFW  
 hu-ACE NMWAQTWSNIYDLVVPFSPASMDTTEAMLKQGWTPRRMFKEADDFTSGLLLPVPPEFW  
 mu-ACE NMWAQTWSNIYDLVVPFSPAPNIDATEAMIKQGWTPRRIFKEADNFFTSGLLLPVPPEFW  
 rat-ACE NMWAQTWSNIYDLVVPFSPASPSIDATEAMIKQGWTPRRIFKEADNFFTSGLLLPVPPEFW  
 rb-ACE NMWAQTWSNIYDLVVPFSPASTMDATEAMIKQGWTPRRMFEEADKFFISGLLLPVPPEFW  
 :\*: :\*: :\*: :\*: :\*: :\* . . . :\*: :\*: :\* . . . \*

ace-2 ENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVMTDDFLTAH **HEMGI** IQYDMAYAA  
 hu-ACET NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGIQYFMQYKD  
 mu-ACET NKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDELVIAHHEMGIQYFMQYKD  
 rb-ACET NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNMEDELVVVHEMGIQYFMQYKD  
 hu-ACE NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGIQYFMQYKD  
 mu-ACE NKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDELVIAHHEMGIQYFMQYKD  
 rat-ACE NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMGIQYFMQYKD  
 rb-ACE NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNMEDELVVVHEMGIQYFMQYKD  
 :\*: :\* : :\*: :\*: :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\*

ace-2 QPFLLRNGANEGFHEAVGEIMLSAATPKHLKLSIGLLSPDFQEDNETEINFLKQALATIV  
 hu-ACET LPVALREGANPGFHEAIGDVLALSSTPKHLHSLNLLSSEGGSD-EHDINFLMKMALDKI  
 mu-ACET LPVTFREGANPGFHEAIGDIMALSVSTPKHLYSNLLSTEGSGY-EYDINFLMKMALDKI  
 rb-ACET LPVALREGANPGFHEAIGDVLALSSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI  
 hu-ACE LPVALREGANPGFHEAIGDVLALSSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI  
 mu-ACE LPVTFREGANPGFHEAIGDIMALSVSTPKHLYSNLLSTEGSGY-EYDINFLMKMALDKI  
 rat-ACE LPVTFREGANPGFHEAIGDVLALSSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI  
 rb-ACE LPVALREGANPGFHEAIGDVLALSSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI  
 \* . :\*: :\* :\*: :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\*

ace-2 GTLPFTYMLEKWRWMVFKEGIPKQDQWKKWEMKREIVGVVEPVPHDETYCDPASLFHVS  
 hu-ACET AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 mu-ACET AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 rb-ACET AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 hu-ACE AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 mu-ACE AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 rat-ACE AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 rb-ACE AFIPFSYLVQWRWRVFDGSITKENYNQEWWSRLRLKYQGLCPPVPRSQGDFDPGAKFHI P  
 . :\*: :\*: :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\*

ace-2 NDYSFIRYYTRTLQYQFQFHEALCQAAGHTGPLHKCDI SNSTEAGQKLENMLRLGKSE PWT  
 hu-ACET SSVPIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQLATAMKLGFSRWP  
 mu-ACET ANVPYVRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWP  
 rb-ACET SSVPIRYFVSFIIQFQFHEALCQAAGHTGPLHTCDIYQSKEAGKRLADAMKLGYSKPWP  
 hu-ACE SSVPIRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGQLATAMKLGFSRWP  
 mu-ACE ANVPYVRYFVSFIIQFQFHEALCQAAGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWP  
 rat-ACE ANVPYIRYFISFIIQFQFHEALCQAAGHTGPLYKCDIYQSKEAGKLLADAMKLGYSKQWP  
 rb-ACE SSVPIRYFVSFIIQFQFHEALCQAAGHTGPLHTCDIYQSKEAGKRLADAMKLGYSKPWP  
 . :\*: :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\*

ace-2 LALENVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKVRISLKS  
 hu-ACET EAMQLITGQPNMSASAMLSYFKPLLDWLRTENEL-----HGEK  
 mu-ACET EAMKLITGQPNMSASAMMNYFKPLTEWLV TENRR-----HGET  
 rb-ACET EAMKVITGQPNMSASAMMNYFKPLMDWLLTENGR-----HGEK  
 hu-ACE EAMQLITGQPNMSASAMLSYFKPLLDWLRTENEL-----HGEK  
 mu-ACE EAMKLITGQPNMSASAMMNYFKPLTEWLV TENRR-----HGET  
 rat-ACE EAMKIITGQPNMSASAIMNYFKPLTEWLV TENRR-----HGET  
 rb-ACE EAMKVITGQPNMSASAMMNYFKPLMDWLLTENGR-----HGEK  
 \* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\* :\*

SECRET

LGDKAYEWN DNEMYLF RSSVAYAMQY FLKVK NQMI LFG EEDVRVAN LKPRISNFNFVTA  
 LGWPQYNWTPN-----  
 LGWPEYNWAPN-----  
 LGWFOYTWT PN-----  
 LGWPQYNWTPN-----  
 LGWPEYNWAPN-----  
 LGWPEYTWT PN-----  
 LGWFOYTWT PN-----  
 \*\* \* \* \*

```

PKNVSDIIPRTEVEKAIIRMSRNRINDAFRLNDNSLEFLGIQFTLGPFPNQPPVSLWLIVFG
-----SARSE-----GPLPDSGRVS-----FLGLDLD---AQQARVGQWLLFL
-----TARAE-----GSTAESNRVN-----FLGLYLE---PQARVGQWLLFL
-----SARSE-----GSLPDSGRVN-----FLGMNLD---AQQARVGQWLLFL
-----SARSE-----GPLPDSGRVS-----FLGLDLD---AQQARVGQWLLFL
-----TARAE-----GSTAESNRVN-----FLGLYLE---PQARVGQWLLFL
-----TARAE-----GSLPESNRVN-----FLGMYLE---PQARVGQWLLFL
-----SARSE-----GSLPDSGRVN-----FLGMNLD---AQQARVGQWLLFL
      . : *      . : : .      ***      . : *      * : : *

```

VVMGVIVVGIVLIFTG|RDRKKKNKARSGENPYASIDISKGENNPGFQNTDDVQTSFN  
 GTALLVATLGLSQRFLFSIR-HRSLHRHSHG-----PQFGSEVELRHS-  
 GVALLVATVGLAHLRYLNIRNHHSLRPHRG-----PQFGSEVELRHS-  
 GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS-  
 GTALLVATLGLSQRFLFSIR-HRSLHRHSHG-----PQFGSEVELRHS-  
 GVALLVATVGLAHLRYLNIRNHHSLRPHRG-----PQFGSEVELRHS-  
 GVALLVATVGLAHLRYLNIRNHHSLRPHRG-----PQFGSEVELRHS-  
 GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS-  
 : : : : : \* : : : : \* : : : : \* : : : : \*



```

HUM_tACE -----
HUM_ace MGAASGRRGPGLLLLPLLLLLLPQPALALDPGLQPGNFSADEAGALFAQSYNSSAEQV
DROME_ace -----
ace-2 -----
CE_ace -----

```

HUM ACE -----  
 HUM ACE LFQSVAASWAHDTNITAENARRQEEAALLSQEFAEAWGQKAKELYEPIWQNFTDPQLRRI  
 DROME ACE -----  
 ace-2 -----  
 CE ACE -----

HUM_tACE	-----
HUM_ace	IGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTAKVCLPNKTATCWSLDPDLTNILASSR
DROME_ace	-----
ace-2	-----
CE_ace	-----

HUM ACE	-----
HUM ACE	SYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFDTDTGAYWRSWYNSPTFEDDL
DROME ACE	-----
ace-2	-----
CE ACE	-----

HUM_tACE	-----
HUM_ace	EHLYQQLEPLYLNLHAFVRRALHRRYGDRYINLRGPIPAHLLGDMWAQSWENIYDMVVPF
DROME_ace	-----
ace-2	-----
CE_ace	-----

HUM_tACE	-----
HUM_ACE	PDKPNLDVTSTMLQQGWNATHMFRVAEEFFTSLELSPMPPEFWEGSMLEKPADGREVVCH
DROME_ACE	-----
ace-2	-----
CE ACE	-----

```

HUM_tACE -----
HUM_ACE      ASAWDFYNRKDFRIKQCTRVMTDQLSTVHHMGHIQYYLQYKDLPVSLRRGANPGFHEAI
DROME_ACE    -----
ace-2        -----
CE ACE       -----

```

```

HUM_tACE      -----
HUM_ACE       GDVLALSVS TPEHLHKIGLLDRVTNDTESDIN YLLKMALEKIAFLPFGYLVDQWRWGVFS
DROME_ ACE    -----
ace-2         -----
CE ACE        -----MKFHILLLLLV

```

```

HUM_tACE      -----
HUM_ ACE      GRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVPNVTPYIRYFVSFVLQFQF
DROME_ ACE    -----
ace-2         -----
CE ACE        GACLPVFTQEIKPPELLPADEAPKDPEAVFSEGEPELTDALDTPKNGSVVPVPEPEPKP

```

SECRET

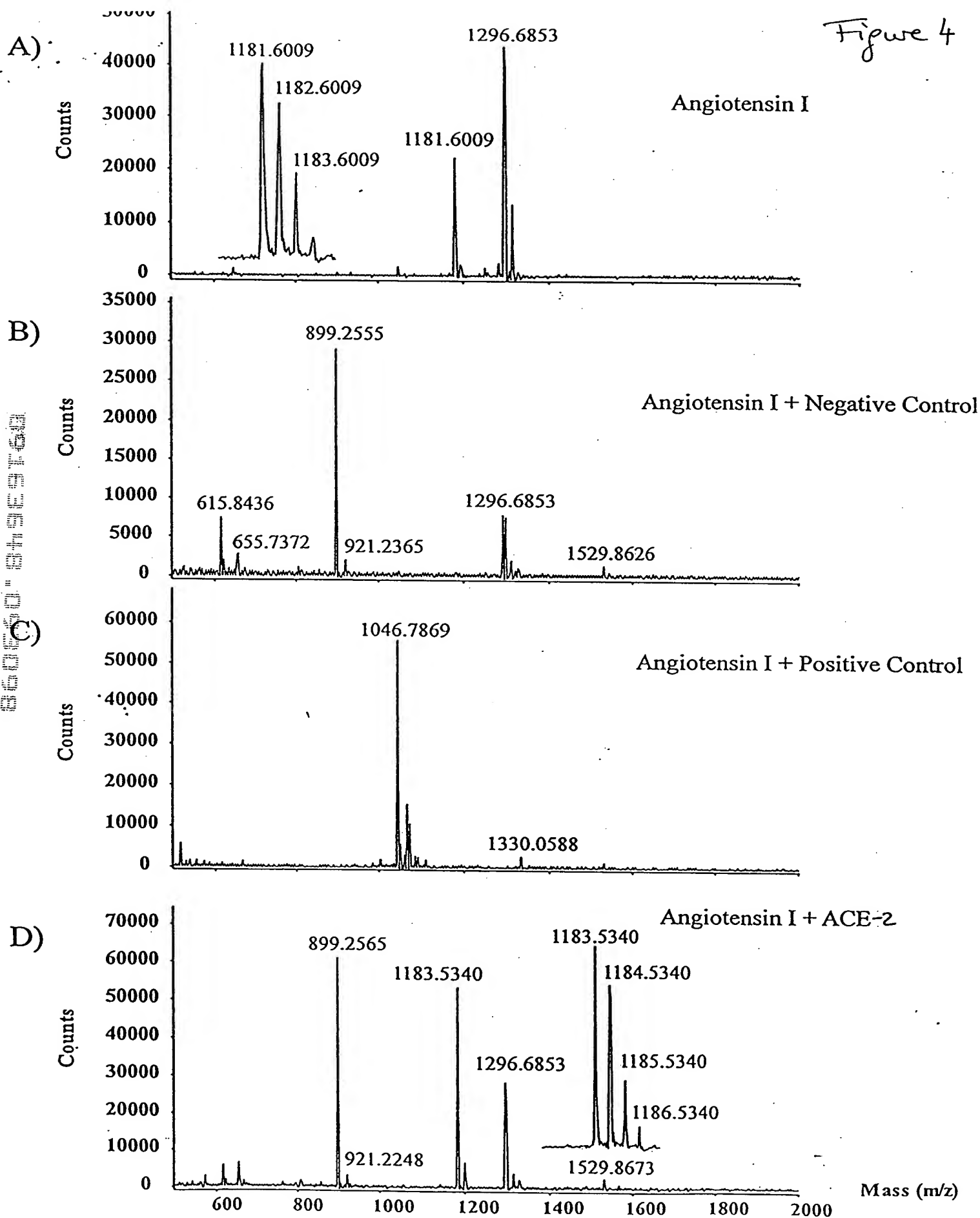




# COPIES

TMD

Figure 4



acehomo2 175 (3.292) Cm (103:276) 1: TOF MSMS 395.40ES+ 310

060660" 849E9T60

Figure 5

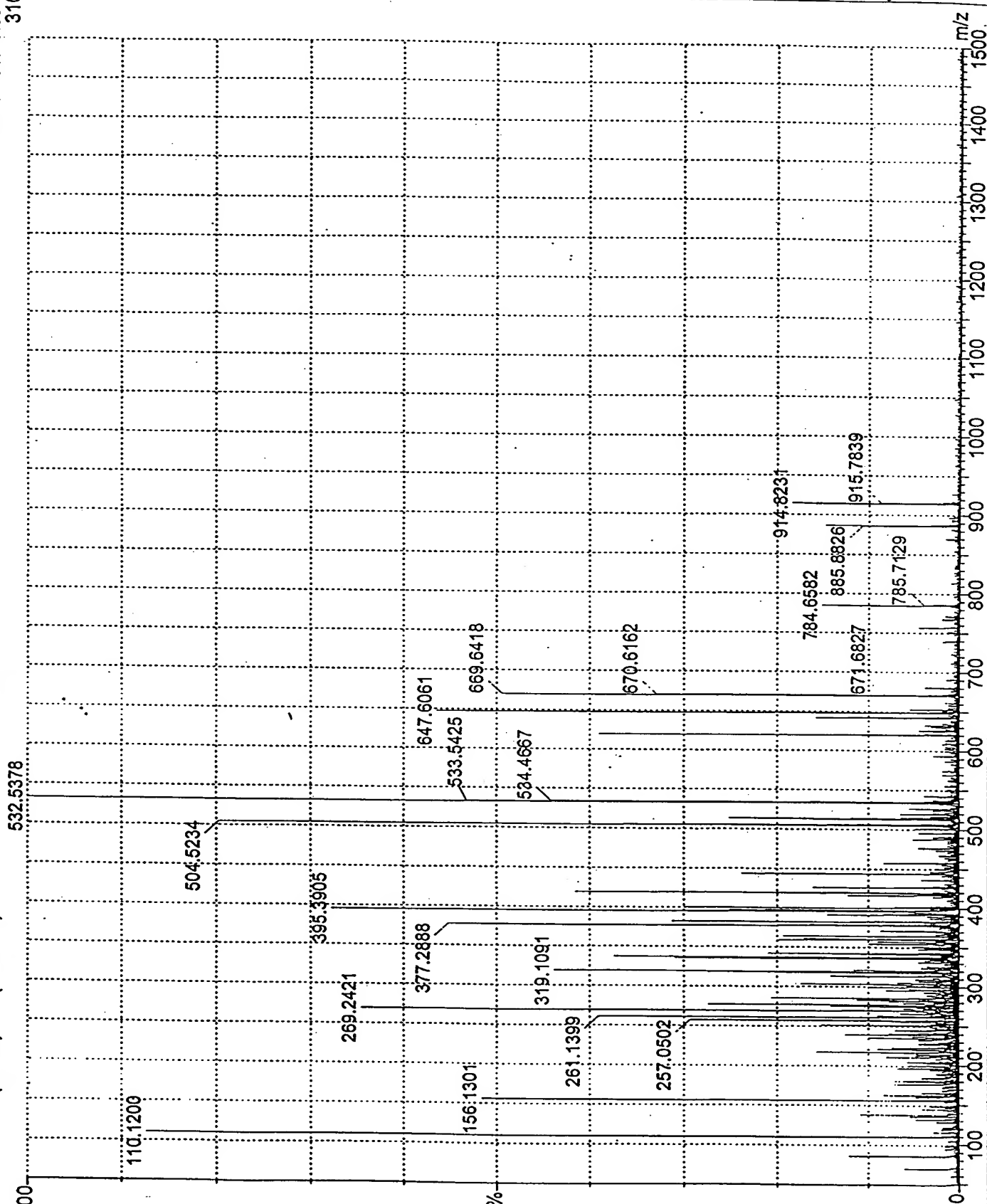
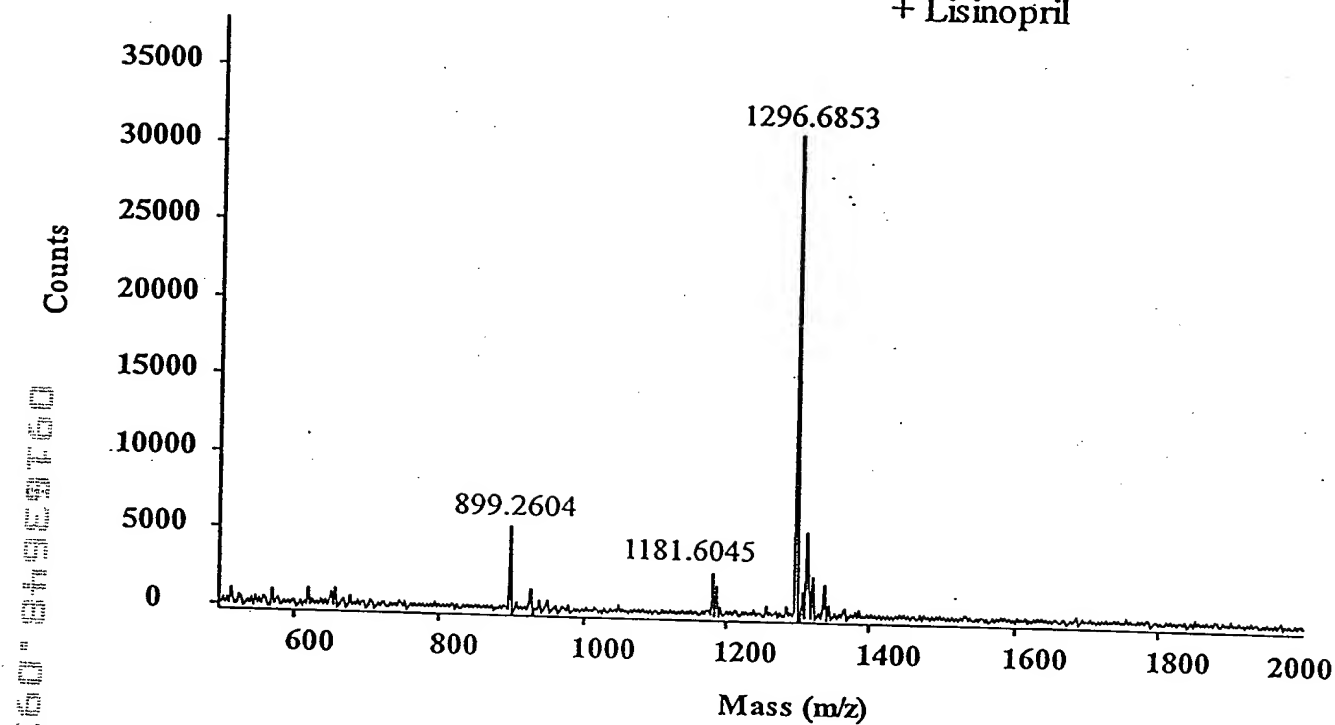


Figure 6

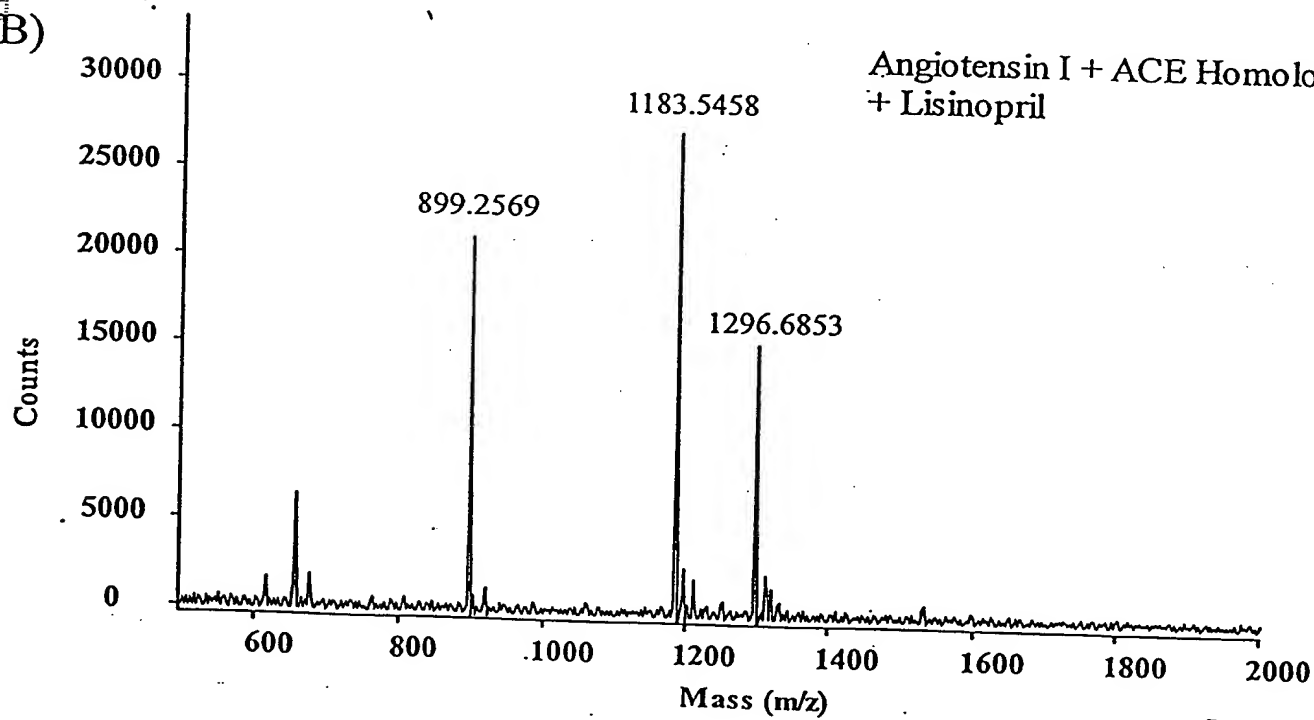
A)

Angiotensin I + Positive Control  
+ Lisinopril



B)

Angiotensin I + ACE Homolog  
+ Lisinopril



# Angiotensin I conversion to products

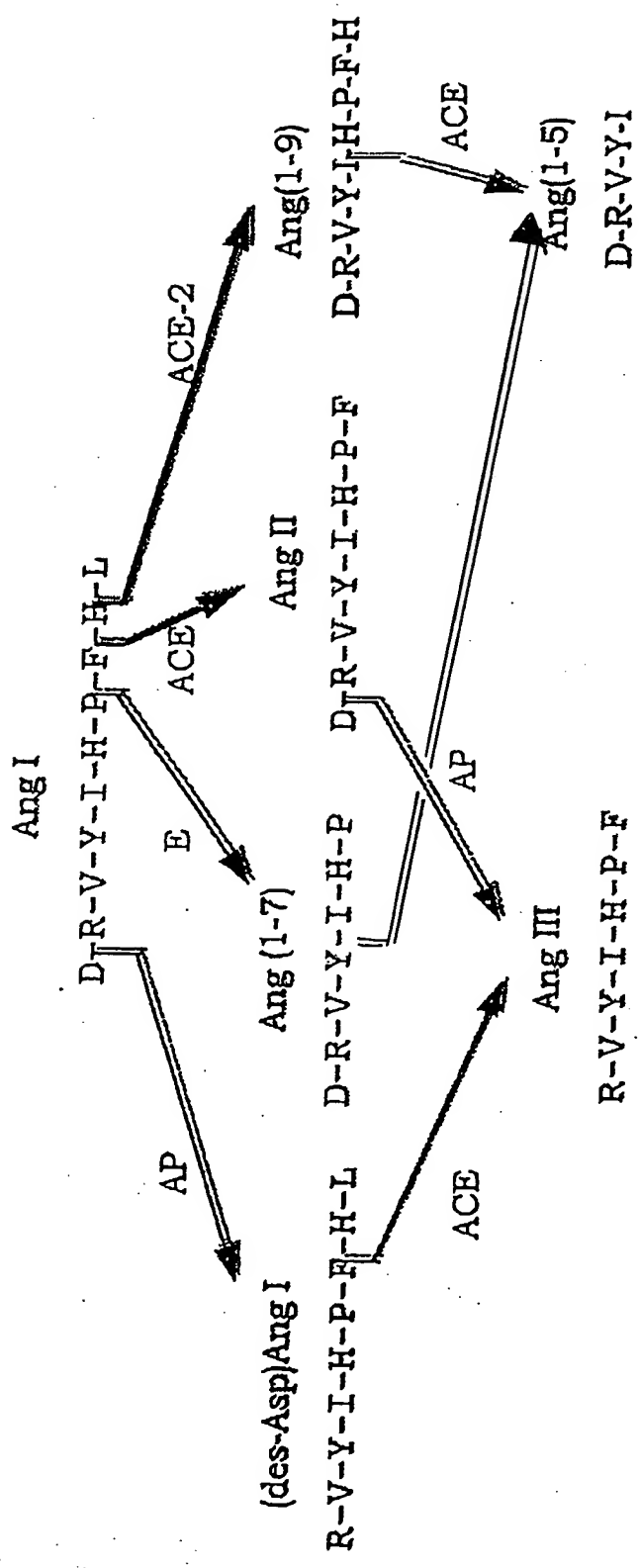


Figure 7.